Claims:

1. An isolated polynucleotide, comprising a polynucleotide sequence selected from the group consisting of

a) polynucleotide which is at least 70% identical to a polynucleotide that codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

b) polynucleotide which codes for a polypeptide that comprises an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID No. 2,

c) polynucleotide which is complementary to the polynucleotides of a) or b), and

d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide of claim 1, DNA which is capable of replication in coryneform bacteria.

3. The polynucleotide of claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide of claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

5. The DNA of claim 2 which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i).

6. The polynucleotide sequence of claim 2, which codes for a polypeptide which comprises the amino acid sequence in SEQ ID No. 2.

7. A coryneform bacterium in which the metE gene is enhanced.

8. A coryneform bacterium serving as a host cell, that contains a vector which carries a polynucleotide of claim 1.

9. Escherichia coli strain DHαmcr/pCREmetAE as DSM 14352 deposited at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

10. Escherichia coli strain DHαmcr/pCREmetAEY as DSM 14353 deposited at the Deutsche Sammlung für Mikroorganismen und Zellkulturen [German Collection of Microorganisms and Cell Cultures], Braunschweig, Germany.

11. A process for the fermentative preparation of L-amino acids, comprising:

a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the metE gene or nucleotide sequences which code for it are enhanced;

b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and

c) isolation of the L-amino acid.

12. The process of claim 11, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

13. The process of claim 11, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

14. The process of claim 11, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the metE gene.

15. The process of claim 11, wherein the expression of the polynucleotide(s) which code(s) for the metE gene is enhanced.

16. The process of claim 11, wherein the catalytic properties of the enzymatic encoded by metE codes are increased.

17. The process of claim 11, wherein for the preparation of L-methionine, coryneform microorganisms have one or more enhanced genes selected from the group consisting of

17.1 the lysC gene which codes for a feed back resistant aspartate kinase,

17.2 the gap gene which codes for glycerolaldehyde 3-phosphate dehydrogenase,

17.3 the pgk gene which codes for 3-phosphoglycerate kinase,

17.4 the pyc gene which codes for pyruvate carboxylase,

17.5 the tpi gene which codes for triose phosphate isomerase

17.6 the metA gene which codes for homoserine O-acetyltransferase

17.7 the metB gene which codes for cystathionine gamma-synthase

17.8 the aecD gene which codes for cystathionine gamma-lyase

17.9 the glyA gene which codes for serine hydroxymethyltransferase

17.10 the metY gene which codes for O-acetylhomoserine sulfhydrylase.

18. The process of claim 11, wherein for the preparation of L-methionine, the coryneform microorganisms have one or more attenuated genes selected from the group consisting of

18.1 the thrB gene which codes for homoserine kinase

18.2 the ilvA gene which codes for threonine dehydratase

18.3 the thrC gene which codes for threonine synthase

18.4 the ddh gene which codes for meso-diaminopimelate D-dehydrogenase

18.5 the pck gene which codes for phosphoenol pyruvate carboxykinase

18.6 the pgi gene which codes for glucose 6-phosphate isomerase

18.7 the poxB gene which codes for pyruvate oxidase.

19. The process of claim 11, wherein microorganisms of the species Corynebacterium glutamicum are employed.

20. The process of claim 19, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetAE is employed.

21. The process of claim 19, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetAEY is employed.

22. A process for preparing an L-methionine-containing animal feedstuffs additive comprising:

a) culture and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth (concentration);

c) removal of an amount of 0 to 100 wt.% of the biomass formed during the fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c) to obtain the animal feedstuffs additive in the desired powder or granule form.

23. The process of claim 22, wherein microorganisms in which further genes of the biosynthesis pathway of L-methionine are additionally enhanced are employed.

24. The process of claim 22, wherein microorganisms are employed in which the metabolic pathways which reduce the formation of L-methionine are at least partly eliminated are employed.

25. The process of claim 22, wherein expression of the polynucleotides which code for the metE gene is enhanced.

26. The process of claim 22, wherein microorganisms of the species Corynebacterium glutamicum are employed.

27. The process of claim 26, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetAE is employed.

28. The process of claim 26, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetAEY is employed.

29. The process of claim 22, wherein one or more of the following steps are additionally carried out:

e) addition of one or more organic substances, including L-methionine and/or D-methionine and/or the racemic mixture D,L-methionine, to the products obtained according to b), c) and/or d);

f) addition of auxiliary substances selected from the group consisting of silicas, silicates, stearates, grits and bran to the substances obtained according to b) to e) for stabilization and to increase storability; or

g) conversion of the substances obtained according to b) to f) into a form stable in rumen, by coating them with film-forming agents.

30. The process of claim 29, wherein a portion of the biomass is removed.

31. The process of claim 30, wherein essentially 100% of the biomass is removed.

32. The process of claim 29, wherein the water content is up to 5 wt.%.

33. The process of claim 32, wherein the water content is less than 2 wt.%.

34. The process of claim 29, wherein the film-forming agents are metal carbonates, silicas, silicates, alginates, stearates, starches, gums or cellulose ethers.

35. An animal feedstuffs additive prepared as claimed in claim 22.

36. The animal feedstuffs additive of claim 35, which comprises 1 wt.% to 80 wt.% L-methionine, D-methionine, D,L-methionine or a mixture thereof, based on the dry weight of the animal feedstuffs additive.

37. A process for obtaining RNA, cDNA or DNA in order to isolate nucleic acids, or polynucleotides or genes which code for homocysteine methyltransferase I or have a high similarity to the sequence of the homocysteine methyltransferase I gene, which comprises employing the polynucleotide sequences of claim 1, as hybridization probes.